



0870  
0824

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/931,009

Source: O/PE

Date Processed by STIC: 8/27/2001

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.**

**FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.**

**PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:**

### **Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

**Checker Version 3.0 can be down loaded from the USPTO website at the following address:**  
**<http://www.uspto.gov/web/offices/pac/checker>**

OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/931,009

DATE: 08/27/2001  
TIME: 12:32:12

Input Set : A:\Sequence Listing.txt  
Output Set: N:\CRF3\08272001\I931009.raw

5 <110> APPLICANT: Smith, Theresa H.  
W--> 6 <120> TITLE OF INVENTION: PRO-INFLAMMATORY FIBRINOPEPTIDE  
W--> 7 <130> FILE REFERENCE: US 1257/01 (VA)  
W--> 8 <140> CURRENT APPLICATION NUMBER:  
C--> 9 <141> CURRENT FILING DATE: 2001-08-17  
W--> 9 <150> PRIOR APPLICATION NUMBER:  
W--> 10 <151> PRIOR FILING DATE:  
W--> 11 <160> NUMBER OF SEQ ID: 2

## ERRORED SEQUENCES

W--> 12 <210> SEQ ID NO: 1  
13 <211> LENGTH: 620  
14 <212> TYPE: PRT  
W--> 15 <213> ORGANISM:  
W--> 16 <220> FEATURE:  
W--> 17 <221> NAME/KEY:  
18 <222> LOCATION:  
19 <223> OTHER INFORMATION: STRANDEDNESS: single  
20 TOPOLOGY: both  
E--> 23 <400> SEQUENCE: 0

Does Not Comply  
Corrected Diskette Needed

All following pages  
for explanation

Please  
consult  
Sequence Rules  
for valid  
format

24	Ala	Asp	Ser	Gly	Glu	Asp	Phe	Leu	Ala	Glu	Gly	Gly	Val		
25				5				10					15		
27	Arg	Gly	Pro	Arg	Val	Val	Glu	Arg	His	Gln	Ser	Ala	Cys	Lys	Asp
28				20			25						30		
30	Ser	Asp	Trp	Pro	Phe	Cys	Ser	Asp	Glu	Asp	Trp	Asn	Tyr	Lys	Cys
31				35			40						45		
33	Pro	Ser	Gly	Cys	Arg	Met	Lys	Gly	Leu	Ile	Asp	Glu	Val	Asn	Gln
34				50			55						60		
36	Asp	Phe	Thr	Asn	Arg	Ile	Asn	Lys	Leu	Lys	Asn	Ser	Leu	Phe	Glu
37				65			70						75		
39	Tyr	Gln	Lys	Asn	Asn	Lys	Asp	Ser	His	Ser	Leu	Thr	Thr	Asn	Ile
40				80			85						90		
42	Met	Glu	Ile	Leu	Arg	Gly	Asp	Phe	Ser	Ser	Ala	Asn	Asn	Arg	Asp
43				95			100						105		
45	Asn	Thr	Tyr	Asn	Arg	Val	Ser	Glu	Asp	Leu	Arg	Ser	Arg	Ile	Glu
46				110			115						120		
48	Val	Leu	Lys	Arg	Lys	Val	Ile	Glu	Lys	Val	Gln	His	Ile	Gln	Leu
49				125			130						135		
51	Leu	Gln	Lys	Asn	Val	Arg	Ala	Gln	Leu	Val	Asp	Met	Lys	Arg	Leu
52				140			145						150		
54	Glu	Val	Asp	Ile	Asp	Ile	Lys	Ile	Arg	Ser	Cys	Arg	Gly	Ser	Cys
55				155			160						165		
57	Ser	Arg	Ala	Leu	Ala	Arg	Glu	Val	Asp	Leu	Lys	Asp	Tyr	Glu	Asp
58				170			175						180		
60	Gln	Gln	Lys	Gln	Leu	Glu	Gln	Val	Ile	Ala	Lys	Asp	Leu	Leu	Pro

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SEQUENCE LISTING

<110> Smith, Theresa H.  
<120> PRO-INFLAMMATORY FIBRINOPEPTIDE  
<130> US 1257/01 (VA)

<140>

<150>

<151>

<160> 2

<210> 1

<211> 620

<212> PRT

<213> mandatory response needed -

see item 11 on Env  
summary sheet

<220>

<221>

<222>

<223> ~~STRANDEDNESS: single~~  
~~TOPOLOGY: both~~

not used in new Sequence Rule  
format  
delete

<400> SEQ-ID-NO: 1

Ala Asp Ser Gly Glu Gly Asp Phe Leu Ala Glu Gly Gly Val  
5 10 15

Arg Gly Pro Arg Val Val Glu Arg His Gln Ser Ala Cys Lys Asp  
20 25 30

Ser Asp Trp Pro Phe Cys Ser Asp Glu Asp Trp Asn Tyr Lys Cys  
35 40 45

Pro Ser Gly Cys Arg Met Lys Gly Leu Ile Asp Glu Val Asn Gln  
50 55 60

Asp Phe Thr Asn Arg Ile Asn Lys Leu Lys Asn Ser Leu Phe Glu  
65 70 75

Tyr Gln Lys Asn Asn Lys Asp Ser His Ser Leu Thr Thr Asn Ile  
80 85 90

Met Glu Ile Leu Arg Gly Asp Phe Ser Ser Ala Asn Asn Arg Asp  
95 100 105

Asn Thr Tyr Asn Arg Val Ser Glu Asp Leu Arg Ser Arg Ile Glu  
110 115 120

Val Leu Lys Arg Lys Val Ile Glu Lys Val Gln His Ile Gln Leu  
125 130 135

Leu Gln Lys Asn Val Arg Ala Gln Leu Val Asp Met Lys Arg Leu  
140 145 150

Glu Val Asp Ile Asp Ile Lys Ile Arg Ser Cys Arg Gly Ser Cys  
155 160 165

Ser Arg Ala Leu Ala Arg Glu Val Asp Leu Lys Asp Tyr Glu Asp

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170

175

180

Gln Gln Lys Gln Leu Glu Gln Val Ile Ala Lys Asp Leu Leu Pro  
185 190 195

Ser Arg Asp Arg Gln His Leu Pro Leu Ile Lys Met Lys Pro Val  
200 205 210

Pro Asp Leu Val Pro Gly Asn Phe Lys Ser Gln Leu Gln Lys Val  
215 220 225

Pro Pro Glu Trp Lys Ala Leu Thr Asp Met Pro Gln Met Arg Met  
230 235 240

Glu Leu Glu Arg Pro Gly Gly Asn Glu Ile Thr Arg Gly Gly Ser  
245 250 255

Thr Ser Tyr Gly Thr Gly Ser Glu Thr Glu Ser Pro Arg Asn Pro  
260 265 270

Ser Ser Ala Gly Ser Trp Asn Ser Gly Ser Ser Gly Pro Gly Ser  
275 280 285

Thr Gly Asn Arg Asn Pro Gly Ser Ser Gly Thr Gly Gly Thr Ala  
290 295 300

Thr Trp Lys Pro Gly Ser Ser Gly Pro Gly Ser Thr Gly Ser Trp  
305 310 315

Asn Ser Gly Ser Ser Gly Thr Gly Ser Thr Gly Asn Gln Asn Pro  
320 325 330

Gly Ser Pro Arg Pro Gly Ser Thr Gly Thr Trp Asn Pro Gly Ser  
335 340 345

Ser Glu Arg Gly Ser Ala Gly His Trp Thr Ser Glu Ser Ser Val  
350 355 360

Ser Gly Ser Thr Gly Gln Trp His Ser Glu Ser Gly Ser Phe Arg  
365 370 375

Pro Asp Ser Pro Gly Ser Gly Asn Ala Arg Pro Asn Asn Pro Asp  
380 385 390

Trp Gly Thr Phe Glu Glu Val Ser Gly Asn Val Ser Pro Gly Thr  
395 400 405

Arg Arg Glu Tyr His Thr Glu Lys Leu Val Thr Ser Lys Gly Asp  
410 415 420

Lys Glu Leu Arg Thr Gly Lys Glu Lys Val Thr Ser Gly Ser Thr  
425 430 435

Thr Thr Thr Arg Arg Ser Cys Ser Lys Thr Val Thr Lys Thr Val  
440 445 450

Ile Gly Pro Asp Gly His Lys Glu Val Thr Lys Glu Val Val Thr

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455	460	465
Ser Glu Asp Gly Ser Asp Cys Pro Glu Ala Met Asp Leu Gly Thr		
470	475	480
Leu Ser Gly Ile Gly Thr Leu Asp Gly Phe Arg His Arg His Pro		
485	490	495
Asp Glu Ala Ala Phe Phe Asp Thr Ala Ser Thr Gly Lys Thr Phe		
500	505	510
Pro Gly Phe Phe Ser Pro Met Leu Gly Glu Phe Val Ser Glu Thr		
515	520	525
Glu Ser Arg Gly Ser Glu Ser Gly Ile Phe Thr Asn Thr Lys Glu		
530	535	540
Ser Ser Ser His His Pro Gly Ile Ala Glu Phe Pro Ser Arg Gly		
545	550	555
Lys Ser Ser Ser Tyr Ser Lys Gln Phe Thr Ser Ser Thr Ser Tyr		
560	565	570
Asn Arg Gly Asp Ser Thr Phe Glu Ser Lys Ser Tyr Lys Met Ala		
575	580	585
Asp Glu Ala Gly Ser Glu Ala Asp His Glu Gly Thr His Ser Thr		
590	595	600
Lys Arg Gly His Ala Lys Ser Arg Pro Val Arg Gly Ile His Thr		
605	610	615
Ser Pho Leu Gly Lys		
620		

<210> 2  
<211> 4  
<212> PRT  
<213> Artificial Sequence  
<220>  
<221>  
<222>  
<223> DESCRIPTION OF ARTIFICIAL SEQUENCE: peptide  
STRANDEDNESS: single  
TOPOLOGY: linear delete  
<400> SEQ ID NO: 2  
Gly Pro Arg Pro

insufficient explanation  
for Artificial Sequence;  
give source of  
genetic material  
(see item 11 on  
Error Summary  
sheet)

**Raw Sequence Listing Error Summary**

**ERROR DETECTED**

**SUGGESTED CORRECTION**

**SERIAL NUMBER:** 09/931,009

**ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE**

- 1  Wrapped Nucleic  
Wrapped Aminos
 

The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2  Invalid Line Length
 

The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3  Misaligned Amino  
Numbering
 

The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4  Non-ASCII
 

The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5  Variable Length
 

Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6  PatentIn 2.0  
"bug"
 

A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7  Skipped Sequences  
(OLD RULES)
 

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8  Skipped Sequences  
(NEW RULES)
 

Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9  Use of n's or Xaa's  
(NEW RULES)
 

Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10  Invalid <213>  
Response
 

Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11  Use of <220>
 

Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

*PSI* →
- 12  PatentIn 2.0  
"bug"
 

Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13  Misuse of n
 

n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.